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 GCTGCGGAATTCTAACGACTCACTATAGGGAGTCGACCCACGCGTCCGGTGGCAGGCCGGGGTGAGGGCTCGGC  
 TCCGGGAGCTGCACGGGCTGCGTGGAAAGAGCGCCGAGCGGTGGCGTGGTGCCTCCCTCCCTCGTCGGAAAGAATC

START SEQ ID NO:2

M P A	3
GTTGGTCTCCTGCCGTGCCGGATCCAGTCAGAAGTCCAGCCTGCCACTGTTCTGATGCC	ATG CCA GCA

START SEQ ID NO:3

P T Q L F F P L I R N C E L S R I Y G T	23
CCA ACT CAA CTG TTT CCT CTC ATC CGT AAC TGT GAA CTG AGC AGG ATC TAT GGC ACT	69

A C Y C H H K H L C C S S S Y I P Q S R	43
GCA TGT TAC TGC CAC CAC AAA CAT CTC TGT TGT TCC TCA TCG TAC ATT CCT CAG AGT CGA	129

L R Y T P H P A Y A T F C R P K E N W W	63
CTG AGA TAC ACA CCT CAT CCA GCA TAT GCT ACC TTT TGC AGG CCA AAG GAG AAC TGG TGG	189

Q Y T Q G R R Y A S T P Q K F Y L T P P	83
CAG TAC ACC CAA GGA AGG AGA TAT GCT TCC ACA CCA CAG AAA TTT TAC CTC ACA CCT CCA	249

Q V N S I L K A N E Y S F K V P E F D G	103
CAA GTC AAT AGC ATC CTT AAA GCT AAT GAA TAC AGT TTC AAA GTG CCA GAA TTT GAC GGC	309

K N V S S I L G F D S N Q L P A N A P I	123
AAA AAT GTC AGT TCT ATC CTT GGA TTT GAC AGC AAT CAG CTG CCT GCA AAT GCA CCC ATT	369

E D R R S A A T C L Q T R G M L L G V F	143
GAG GAC CGG AGA AGT GCA GCA ACC TGC TTG CAG ACC AGA GGG ATG CTT TTG GGG GTT TTT	429

D G H A G C A C S Q A V S E R L F Y Y I	163
GAT GGC CAT GCA GGT TGT GCT TCC CAG GCA GTC AGT GAA AGA CTC TTT TAT TAT ATT	489

A V S L L P H E T L L E I E N A V E S G	183
GCT GTC TCT TTG TTA CCC CAT GAG ACT TTG CTA GAG ATT GAA AAT GCA GTG GAG AGC GGC	549

R A L L P I L Q W H K H P N D Y F S K E	203
CGG GCA CTG CTA CCC ATT CTC CAG TGG CAC AAG CAC CCC AAT GAT TAC TTT AGT AAG GAG	609

A S K L Y F N S L R T Y W Q E L I D L N	223
GCA TCC AAA TTG TAC TTT AAC AGC TTG AGG ACT TAC TGG CAA GAG CTT ATA GAC CTC AAC	669

T G E S T D I D V K E A L I N A F K R L	243
ACT GGT GAG TCG ACT GAT ATT GAT GTT AAG GAG GCT CTA ATT AAT GCC TTC AAG AGG CTT	729

D N D I S L E A Q V G D P N S F L N Y L	263
GAT AAT GAC ATC TCC TTG GAG GCG CAA GTT GGT GAT CCT AAT TCT TTT CTC AAC TAC CTG	789

V L R V A F S G A T A C V A H V D G V D	283
GTC CTT CGA GTG GCA TTT TCT GGA GCC ACT GCT TGT GTG GCC CAT GTG GAT GGT GTT GAC	849

L H V A N T G D S R A M L G V Q E E D G	303
CTT CAT GTG GCC AAT ACT GGC GAT AGC AGA GCC ATG CTG GGT GTG CAG GAA GAG GAC GGC	909

Fig. 1A

S W S A V T L S N D H N A Q N E R E L E 323  
 TCA TGG TCA GCA GTC ACG CTG TCT AAT GAC CAC AAT GCT CAA AAT GAA AGA GAA CTA GAA 969

R L K L E H P K S E A K S V V K Q D R L 343  
 CGG CTG AAA TTG GAA CAT CCA AAG AGT GAG GCC AAG AGT GTC GTG AAA CAG GAT CGG CTG 1029

L G L L M P F R A F G D V K F K W S I D 363  
 CTT GGC TTG CTG ATG CCA TTT AGG GCA TTT GGA GAT GTA AAG TTC AAA TGG AGC ATT GAC 1089

L Q K R V I E S G P D Q L N D N E Y T K 383  
 CTT CAA AAG AGA GTG ATA GAA TCT GGC CCA GAC CAG TTG AAT GAC AAT GAA TAT ACC AAG 1149

F I P P N Y H T P P Y L T A E P E V T Y 403  
 TTT ATT CCT CCT AAT TAT CAC ACA CCT TAT CTC ACT GCT GAG CCA GAG GTA ACT TAC 1209

H R L R P Q D K F L V L A T D G L W E T 423  
 CAC CGA TTA AGG CCA CAG GAT AAG TTT CTG GTG TTG GCT ACT GAT GGG TTG TGG GAG ACT 1269

M H R Q D V V R I V G E Y L T G M H H Q 443  
 ATG CAT AGG CAG GAT GTG GTT AGG ATT GTG GGT GAG TAC CTA ACT GGC ATG CAT CAC CAA 1329

Q P I A V G G Y K V T L G Q M H G L L T 463  
 CAG CCA ATA GCT GTT GGT GGC TAC AAG GTG ACT CTG GGA CAG ATG CAT GGC CTT TTA ACA 1389

E R R T K M S S V F E D Q N A A T H L I 483  
 GAA AGG AGA ACC AAA ATG TCC TCG GTA TTT GAG GAT CAG AAC GCA GCA ACC CAT CTC ATT 1449

R H A V G N N E F G T V D H E R L S K M 503  
 CGC CAC GCT GTG GGC AAC AAC GAG TTT GGG ACT GTT GAT CAT GAG CGC CTC TCT AAA ATG 1509

L S L P E E L A R M Y R D D I T I I V V 523  
 CTT AGT CTT CCT GAA GAG CTT GCT CGA ATG TAC AGA GAT GAC ATT ACA ATC ATT GTA GTT 1569

Q F N S H V V G A Y Q N Q F \* END SEQ ID NO:2 538  
 CAG TTC AAT TCT CAT GTT GTA GGG GCG TAT CAA AAC CAA GAA TAG END SEQ ID NO:3 1614

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 GGGTGGCAGGGTCAGGAGAGCTGGTCTGCCTAGCTCAGATTCTAGGCACCTGCACCTGAAGCAAGTCACCTTCTTA  
 TCACAGGTGTCTGAAACATTAGCTTCTTACCAACCTGAGAAAATTAGGATGACCTGGCAAATAAGATCTGAATAG  
 GCCAAAAGCAAGTATCTGCTGTGTAGCTCTGGTAAAGTGAAGAACAGTACTGTTCACACCTTCTCACTGA  
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Fig. 1B

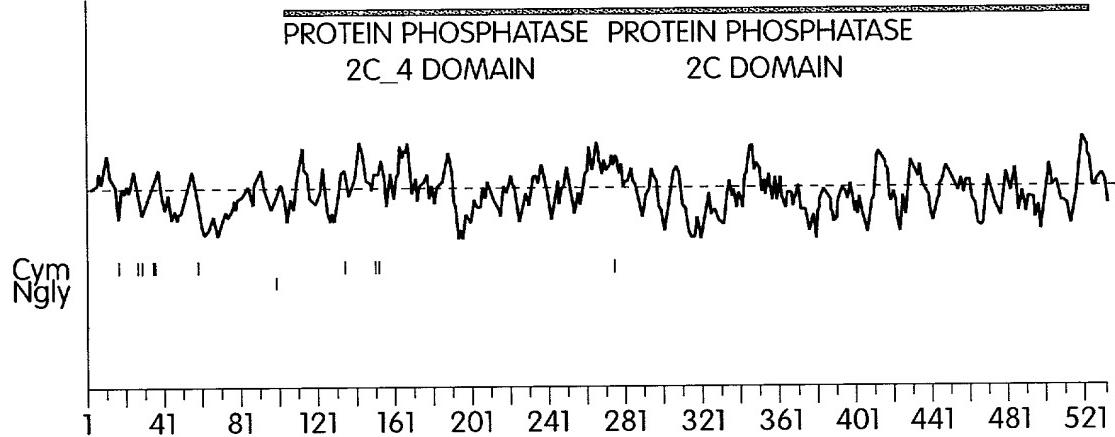


Fig. 2

PP2C: domain 1 of 1, from 173 to 461: score 261.3, E = 1.3e-74

SEQ ID NO:4

\*->ldvgvsrmqgwrksmeDahialknlnsssgkdswsffavfDGhgGs

26583 173 LLEIENAVESGRALLPILQWHKHPNDYF-SKEASKLYFNSLRTYWQE 218 SEQ ID NO:2

1 +++++ + r +++ ++++++ ++ s++ s+ +f + + + +

qaakyagkhkhk.tilaerksfpegdpwEmklsdledalkesfleadtde

+ +g++ +++ + a++ f+ +d+ d + + + ++++++

26583 219 LIDLNTGESTDIDVKEALINAFKRLDN-----DISLEAQVGDPNSFLNY 262

elrsaeasaankvlkedlssGsTAvalirgnkLyVANvGDSRavLcrn

+++ + SG+TA+va+++g +L+VAN+GDSRa+L+ +

26583 263 LVLR-----VAFSGATACTACVAHVDGVDLHVANTGDSRAMLGVQ 299

gnaikw.avtLteDHkPsnedEreRIeaaGGfvsvs...ngRvnGvLav

+++++W+avtL++DH+++ne+E+eR++ +++++ + +S + + +R++G L++

26583 300 EEDGSWsAVTLSNDHNAQNERELERLKLEHPKSEAKSvvkQDRLLGLLMP 349

SRAfGdfelKpgsklgpeas.i.e.a.ny.eyiks.pe.....qlVtaeP

RafGD+++K+ +l+++ ++++++ n++ey+k+ p++ +++++ taeP

26583 350 FRAFGDVFKFKWSIDLQKRVleSgPdQ1NDnEYTKFiPPnyhtpPYLTAE 399

dvtssstdltpdkDeFlilAcDGLWDvvsdqevvdivrselsdgnksaedp

+vt + + + l+p+ D+F1+LA+DGLW++++ q+vv iv + l+ + +

26583 400 EVT-YHRLRPQ-DKFLVLATDGLWETMHRQDVVRIVGEYL TGM-----H 441

meaaeklvdeaiargaeDni<-\*

++ ++ + + g ++

26583 442 HQQPIAVGGYKVTLGQMHG 461

Fig. 3A

PP2C\_4: domain 1 of 1, from 99 to 523: score 338.5, E = 7.6e-98

SEQ ID NO:5

\*->es.sgknlglyglgessmqqwrkpmEDahvirp.....ffgvfD  
 + gkn +++ g+ +s++ +++ p+ED+ ++ + +++++ + gVfD

26583 99 PEfDGKVNSSILGF-DSNQLPANAPIEDRRSAATc1qtrgmlLGVFD 144 SEQ ID NO:2

GHGGseaakflsknlheilaelsfdkdeslkene.e.lk.d.ep.....  
 GH+G +++ +s++l ++a +l +++ ++ en+ e+++ + ++ + ++

26583 145 GHAGCACSQAVSERLFYYIAVSILLPHETLLEIENAvEsGRaLLPIlqwnk 194

.....ess.e.r.ln.gdksledveealrkaFlrtd  
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26583 195 hpndyfskeasklyfnslrTYWqELIdLNtGESTDIDVKEALINAFKRLD 244

eei.....sTAvalirgnklyvANvGDSRa  
 ++i+ + + +++++ + + + +TA+va+++g +l+vAN+GDSRa

26583 245 NDIsleaqvgdpnsflnylvrlrafsgATACVAHVDGVDLHVANTGDSRA 294

vLcrngkd.swegvrtysavqLteDHkpanedEreRieaaGGevepidre  
 +L+ + +d+sw sav L++DH++ ne+E+eR++ +++++ e +++

26583 295 MLGVQEEDgSW-----SAVTLSDHNAQNERELERLKLEHPKSE--AKS 336

fvsngggvvwRvnGvvisLavsRalGDfelKk.ked.e.lie....en.  
 +v ++ R++G L++ Ra+GD+++K++++++i+e+++++n+

26583 337 VVKQD-----RLLGL---LMPFRAFGDVFKFWsIDLqKrVIEsgpdqLNd 378

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26583 379 NEYTKFIPPNYHTPPYLTAEPETYHRL-----RPQDKFLVLATDGLWE 422

vlsnqeavdivrkhlrkgddk.evksaaqela.r.a.d....s.....  
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26583 423 TMHRQDVVRIVGEYLTGMHHQqPIAVGGYKVTLGqMhG1lteRrtkmssv 472

.....l.r..skkhndpkeaakllvd1Al.....kDNiTvvv  
 +--+ ++l r+ +++++ +--+L +--+ +--+ + +D+iT++v

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V<-\*

V

26583 523 V 523

Fig. 3B

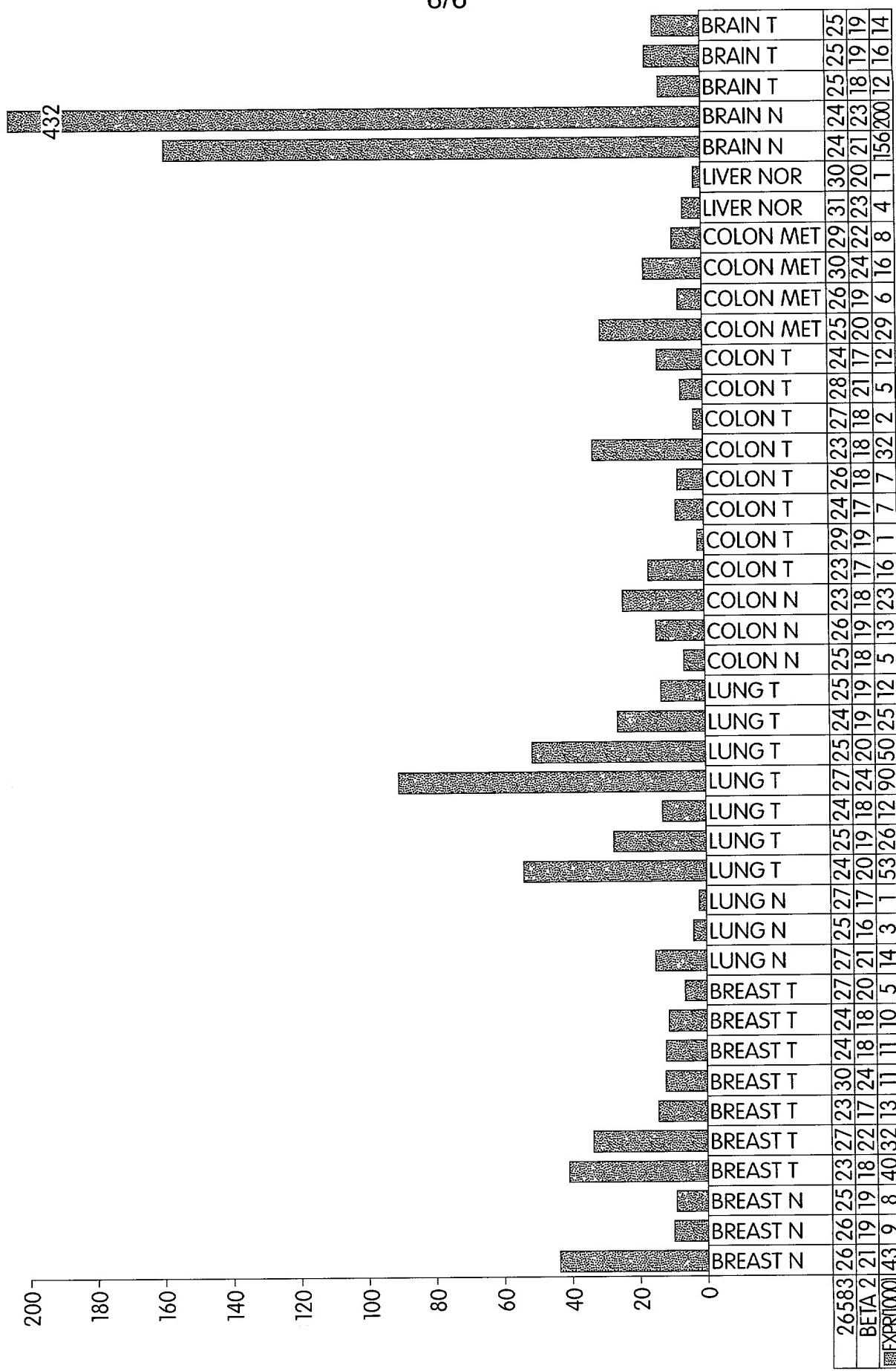


Fig. 4